(FILE 'HOME' ENTERED AT 14:59:10 ON 09 SEP 2003)

FILE 'MEDLINE' ENTERED AT 14:59:19 ON 09 SEP 2003
L1 2 S SITU/TI AND BDNA/TI
L2 2 DUP REM L1 (0 DUPLICATES REMOVED)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE' ENTERED AT 14:59:53 ON 09 SEP 2003
L3 2 S L2
L4 28 S SITU AND BDNA
L5 17 DUP REM L4 (11 DUPLICATES REMOVED)

=>

6027893

L5 ANSWER 13 OF 17 MEDLINE on STN
ACCESSION NUMBER: 1999186097 MEDLINE
DOCUMENT NUMBER: 99186097 PubMed ID: 10086178
TITLE: Branched DNA signal amplification for direct quantitation of nucleic acid sequences in clinical specimens.
AUTHOR: Nolte F S
CORPORATE SOURCE: Department of Pathology and Laboratory Medicine, Emory University School of Medicine, Atlanta, Georgia, USA.
SOURCE: ADVANCES IN CLINICAL CHEMISTRY, (1998) 33 201-35. Ref: 87
Journal code: 2985173R. ISSN: 0065-2423.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals; AIDS
ENTRY MONTH: 199904
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AB In this chapter I have reviewed the development of **bDNA** as a method for quantitation of nucleic acid targets and the application of this technology to the study of infectious diseases and cell biology. The ability to quantify viral nucleic acids in clinical specimens has led to a better understanding of the pathogenesis of chronic viral infections such as HIV-1, HCV, and HBV. The information provided by these methods can also be important in the management of patients with these infections. The prognostic value of a single baseline HIV-1 RNA level rivals that surgical staging procedures for cancer, which are among the most powerfully predictive tests in medicine (Mellors et al., 1996). These methods have been used to assess rapidly the effects of antiviral therapy, which has both expedited the development of antiviral drugs and improved the management of patients with HIV-1 and HCV infections. **bDNA** has several characteristics that distinguish it from the quantitative target amplification systems, including better tolerance of target sequence variability, more direct measurement of target, simpler sample preparation, and less sample-to-sample variation. However, the first- and second-generation **bDNA** assays lacked sensitivity compared with the target amplifications systems. The changes incorporated into the third-generation assays have effectively increased the signal-to-noise ratio to such a high level that the analytical sensitivity of system 8 **bDNA** approaches that of PCR. In theory, **bDNA** can be made even more sensitive by increasing both the sample volume and the signal-to-noise ratio. Nonspecific hybridization can be further reduced by finding more effective blockers for the solid phase or by redesigning the amplifier molecule or the solid phase itself. The increased sensitivity may create new applications for the technology in filter and in **situ** hybridization assays.

L5 ANSWER 8 OF 17 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2001:60063 BIOSIS
DOCUMENT NUMBER: PREV200100060063
TITLE: In **situ** hybridization using the **bDNA** technology.
AUTHOR(S): Antao, Vincent P. (1); Player, Audrey N.; Kolberg, Janice A.
CORPORATE SOURCE: (1) Bayer Diagnostics, 4560 Horton Street, Emeryville, CA, 94608 USA
SOURCE: Patterson, Bruce K.. Techniques in quantification and localization of gene expression, (2000) pp. 81-93. Techniques in quantification and localization of gene expression. print.
Publisher: Birkhaeuser Boston c/o Springer-Verlag New York, Inc., 175 Fifth Avenue, New York, NY, 10010, USA.
ISBN: 0-8176-4034-7 (dos).
DOCUMENT TYPE: Book
LANGUAGE: English
SUMMARY LANGUAGE: English